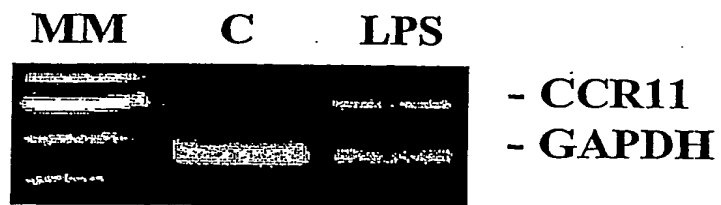


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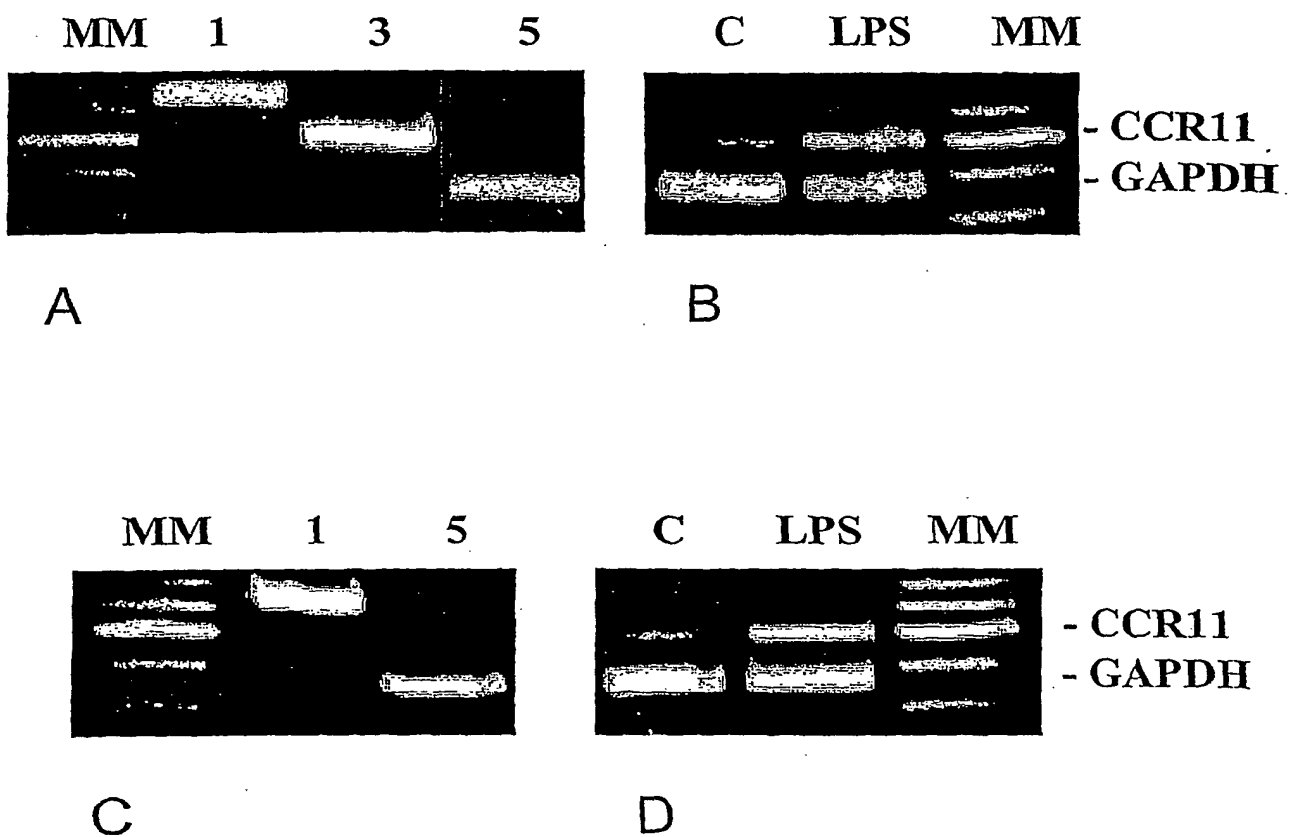
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Fig. 1



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Fig. 2

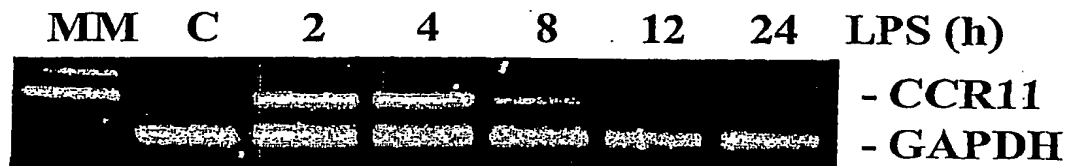


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Fig. 3

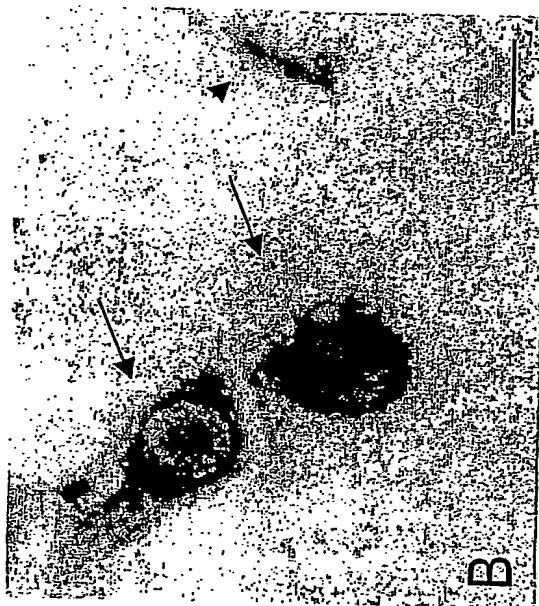


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Fig. 4

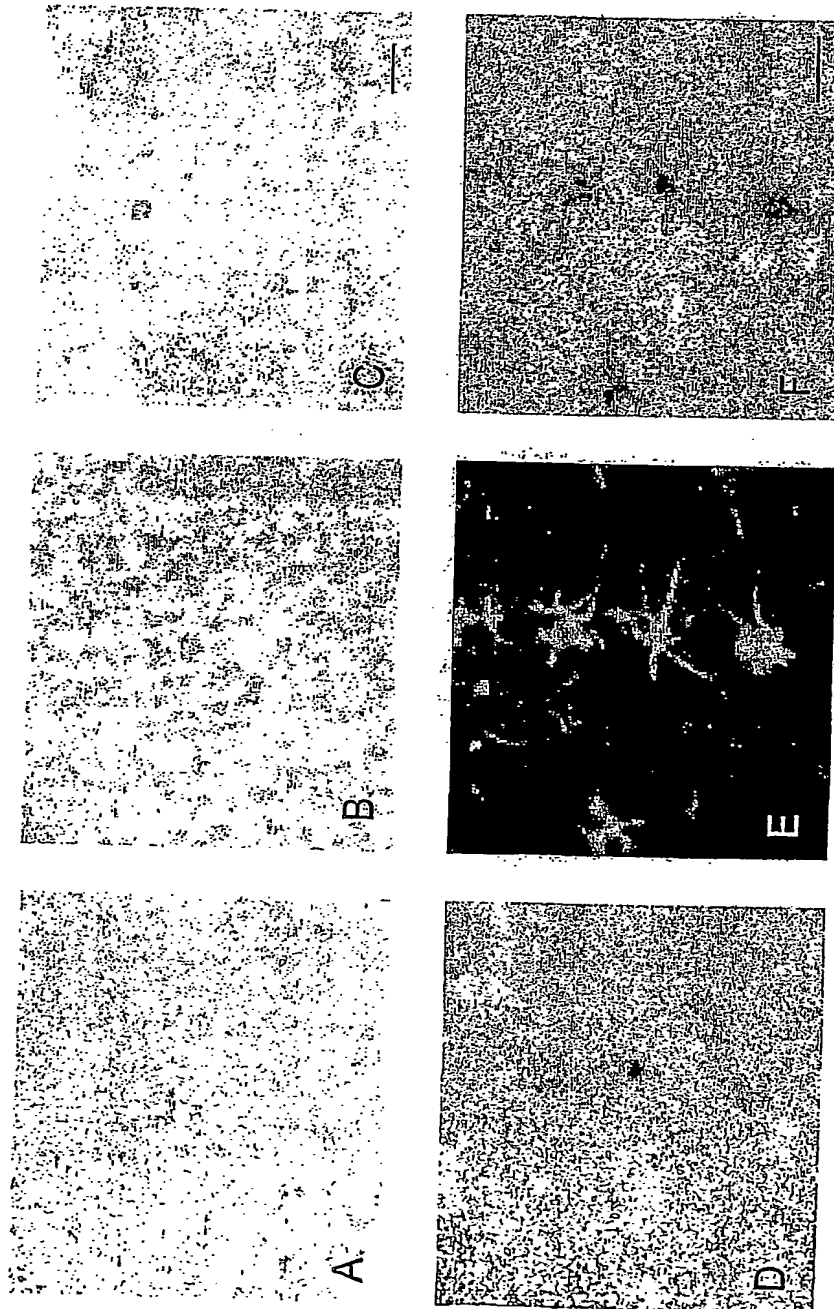


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Fig. 5

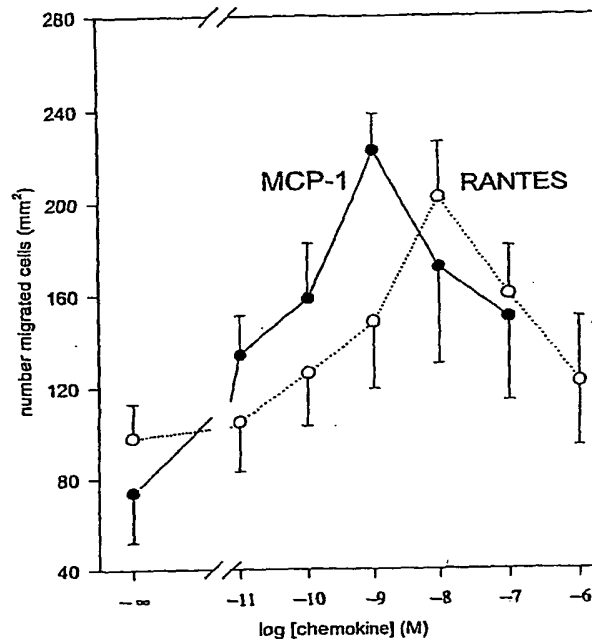


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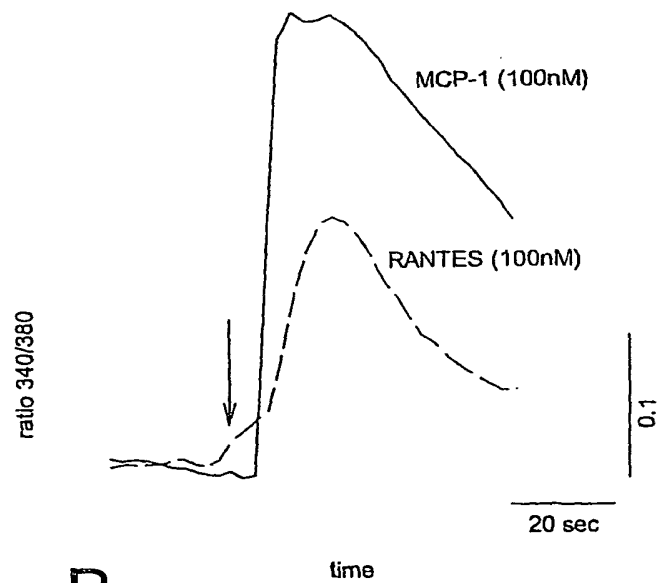
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Fig. 6.



A



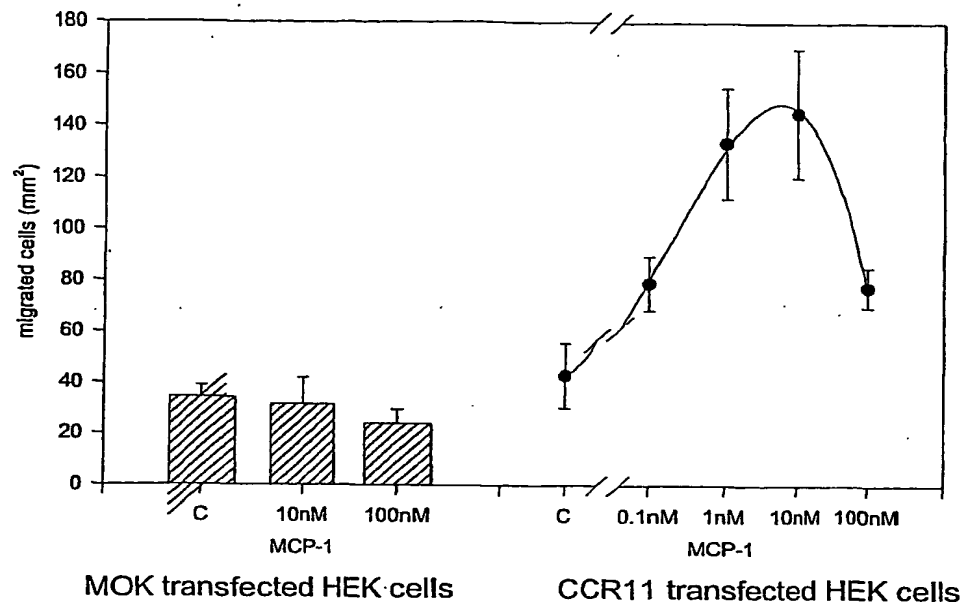
B

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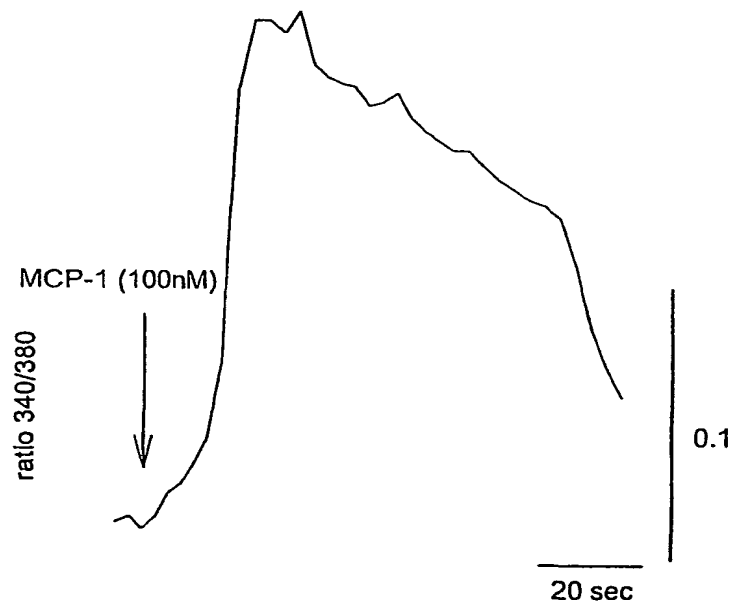
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Fig. 7



A



B

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Fig. 8

CLUSTAL W (1.81) multiple sequence alignment

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hCCR12      ATGGCCAAATTACACGCTGGCACCAGAGGATGAATATGATGTCTCAT---AGAAGGTGAA 57
mCCR12      ATGGATAACTACACAGTGGCCCCGGGACGATGAATATGATGTCTCTAATCTTAGACGACTAC 60
          **** * * * * * **** * * * * * **** * * * * *
hCCR12      CTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCCAGGCACCTCAGCCCCAG 117
mCCR12      CTGGACAACAGTGGGCCGACCAAA-GTTCCG-----GCCCCCGAGTTCCTCTCCCCCCAG 114
          **** * * * * * **** * * * * * **** * * * * *
hCCR12      CTGGTGCCATCAGTCTGCTCTGCTGTGTGTTTGTGATCGGTGTCTCTGGACAATCTCCTGGTT 177
mCCR12      CAGGTGCTGCAGTTCTGCTGCGCGGTGTTTTCGGTGGGTCTCTTGGACAACGTGCTGGCG 174
          * * * * * * * * * * * * * * * * * * * * * *
hCCR12      GTGCTTATCCTGGTAAATATAAAGGACTCAAACCGGTGGAAATATCTATCTTCTAAAC 237
mCCR12      GTGTTTATCTTGGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCTCTAAAC 234
          *** * * * * * * * * * * * * * * * * * * * *
hCCR12      TTGGCAGTTTCTAACTTGTTGTTTCTTGCTTACCCGTGCCCTTCTGGGCTCATGCTG---- 292
mCCR12      CTGGCAGTTTCAAAACCTGTGTGTTTCTGCTTCCCTGCGGTCTCTGGGCCCATCTGCAGCA 294
          **** * * * * * * * * * * * * * * * * * * *
hCCR12      ---GGGGCGATCCC-----ATGTGTAAATTCATTTGGACTGTACTTCGTGGGC 339
mCCR12      CACGGGGAAGCCCTGGCAACGGGACCTGTAAAGTTCTGTGCGACTCCACTCCTCGGGC 354
          **** * * * * * * * * * * * * * * * * * * *
hCCR12      CTGTACAGTGAGACATTTTTCATTTGCCTTCTGACTGTGCAAGGTACCTAGTGTTTTG 399
mCCR12      TTATACAGCGAGGTGTTTTCACAATCCTCCTCCTCTGTGCAAGGATACAGGTGTTT-- 412
          * * * * * * * * * * * * * * * * * * * * *
hCCR12      CACAAGGGCAACTTTTCTCAGCCAGGAGGAGGGTGCCCTGTGGCATCATTAAGTGTGTC 459
mCCR12      CCCAAGGCGACTGGC-CTCCATCTTCACGACAGTGTCTTGTGGTATTGTTGGGTGCATC 471
          * * * * * * * * * * * * * * * * * * * * *

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Fig. 8a

hCCR12	CTGGCATGGGTAAACAGCCATTCTGGCCACTTTGCCTGAATTGGTGGTTTATAAACCTCAG	519
mCCR12	CTGGCATGGGCCATGGCTACTGCGCTCTCTTTGCCGAGTCTGTGTTTATGAGCCTCGG	531
	***** * * * * * ***** * * * * * ***** * * * * *	
hCCR12	ATGGAAGACCCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAG	579
mCCR12	ATGGAAGACACAGAAACACAAGTGTGCCTTTGGCAAACTTCTTGGCCAATCGAAGCG	591
	***** ***** * * * * * ***** * * * * * ***** * * * *	
hCCR12	ACATTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTGGGTCTTGTCTCTCCCTTA	639
mCCR12	CCGCTCTGGAAGTACGTTCTGACGTCAAAAATGATCATCTTGGTACTTGTCTTTCTCTIG	651
	* ***** * ***** * ***** * * * * * ***** * * * *	
hCCR12	TTTATTTTACATTCTCTATGTGCAAAATGAGAAAAACACTAAGGTTTCAGGGAGCAGAGG	699
mCCR12	CTGGTTTTTATAATCTGCTGCAGGCAACTGAGGAGAGGAGAGCTTCAGGGAGAGACAG	711
	* ***** * * * * * ***** * * * * * ***** * * * *	
hCCR12	TATAGCCTTTTCAAGCTTGTGTTTGGCGTAATGGTAGTCTCTCTCTGATGTGGGCGCC	759
mCCR12	TACGACCTCCACAAAGCCGGCTCTTTGTGTCATAACGGGCGTGTCTTTTGTGATGTGGGCGCT	771
	** *** ***** * * * * * ***** * * * * * ***** *****	
hCCR12	TACAAATATTGCATTTTCCGTGCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAG	819
mCCR12	TACAACACTGTGCTTTTCCGTCTGTCTTTCCAGGAACACTTGTCCCTGCAGGATGAGAAG	831
	***** * * * * * ***** * * * * * ***** * * * * *	
hCCR12	AGCAGGTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATGCCACCACCACCTGC	879
mCCR12	AGCAGGTACCACTTGGACGCAAGTGTTCAGGTACACAGCTGGTAGCGACCCACCACCTGC	891
	***** * * * * * ***** * * * * * ***** * * * * *	
hCCR12	TGCATCAACCCCTCTCCTGTATGCGTTTCTTGTATGGGA---CATTTAGCAATACCTCTGC	936
mCCR12	TGCGTCAACCCCGCTGCTCTATTGTCTTCTTGACCGGAGGCCCTTTATGATACCTTCGC	951
	*** ***** * * * * * ***** * * * * * ***** * * * * *	

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Fig. 8b

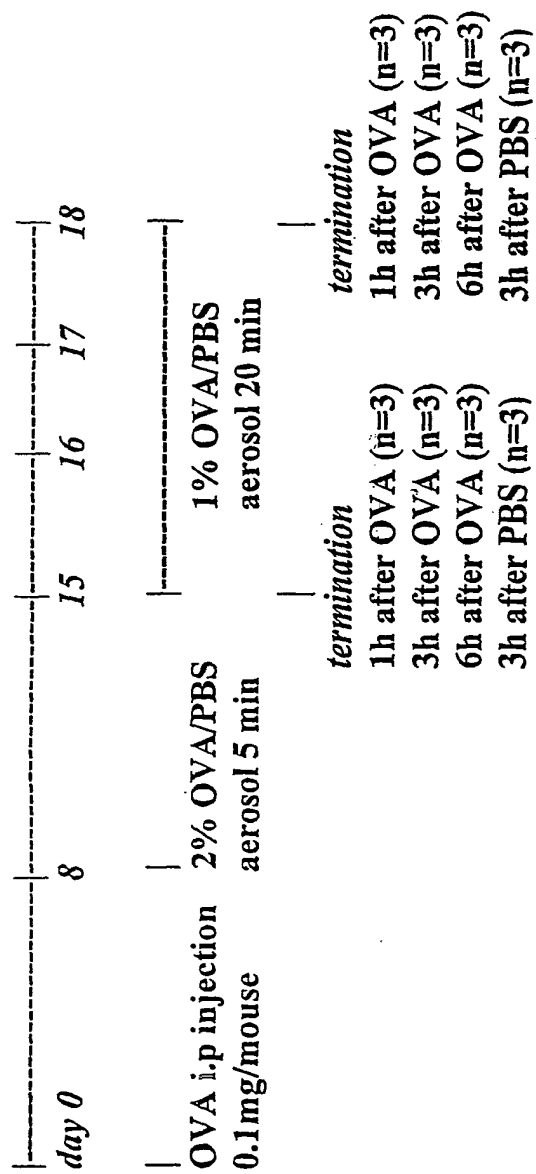
hCCR12	CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGCGAGTCTGCACAAGGC	996
mCCR12	AGCCTGTTCCTCCACGGTGCATGATATCCCTATCAAAAGTAGTGGAGGCTATCAGCAAGCG	1011
	** **** * * * * * * * * * * * * * * * * *	
hCCR12	ACATCGAGGGAAGAACCTGACCATTCCACCGAAGTGTA	1035
mCCR12	CCTCCAAGGGAAGGTGATGGCAGGCCCATTTGAACGTGACAGCAATTGCATCAAGGCAG	1071
	* * ***** * * * * * * * * * * * * * * *	
hCCR12	-----	
mCCR12	GATATAATATAA	1083

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Fig. 9

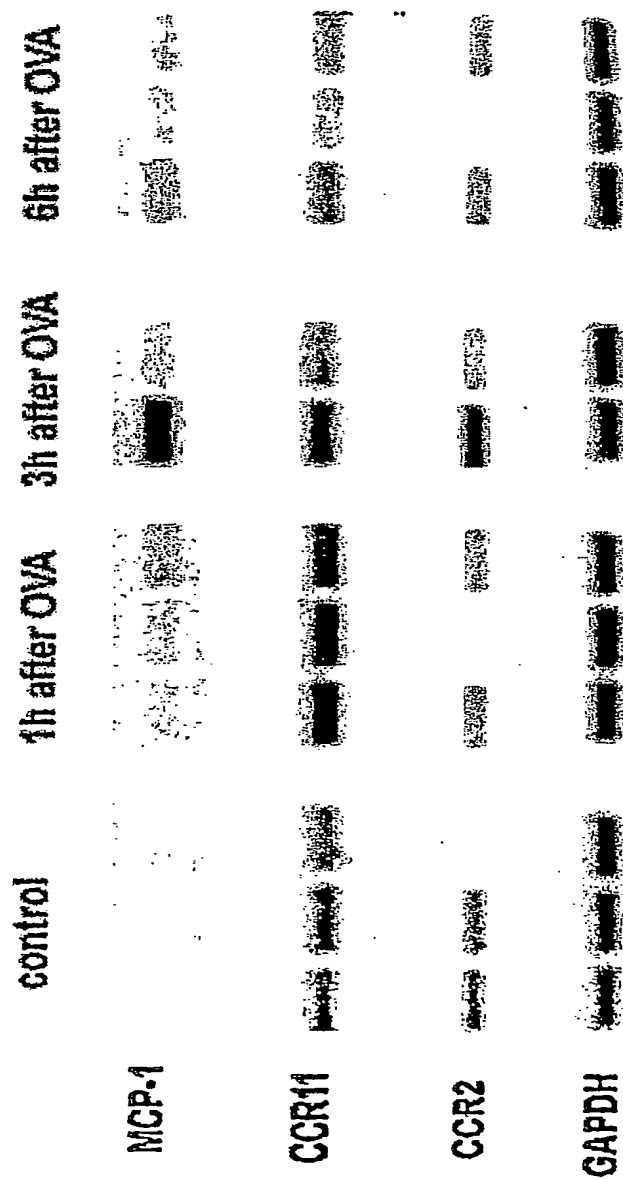


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Fig. 10



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Fig. 11

